REPLACEMENT SHEET

```
     BssHII                        SpeI
  1  GCGCGCGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCA

 57  TTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCC

113  GCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTC

169  CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGACTATTTACGG

                                      NdeI
225  TAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTAT

                    CMV  promotor
281  TGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTAT

                              SnaBI
337  GGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTG

393  ATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATT

449  TCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAAC

505  GGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGG

                              SacI
561  CGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCTCTGGCTAACTAGAGAACCCAC
     ───────────────────────────────▶

                           T7  promotor          HindIII  KpnI
617  TGCTTACTGGCTTATCGAAATTAATACGACTCACTATAGGGAGACCCAAGCTTGGT
                                  ──────────────────▶

                                              SfiI
     AgeI                                     NotI
673  ACCGGTGCGATGGCACCCTGCATGCTGCTCCTGCTGTTGGCGGCCGCCCTGGCCCC
             1▶MetAlaProCysMetLeuLeuLeuLeuLeuAlaAlaAlaLeuAlaPr
                      ApaI
              EcoO109I          AvaI
729  GACTCAGACCCGCGCGGGGGCCCAAAAGCCCGAGGTGATCGATGCCAGCGAGCTGA
     16▶oThrGlnThrArgAlaGlyAlaGlnLysProGluVal I IeAspAlaSerGluLeuT
785  CCCCCGCCGTGACCACCTACAAGCTAGTGATCAACGGCAAGACCCTGAAGGGCGAG
     35▶hrProAlaValThrThrTyrLysLeuVal I IeAsnGlyLysThrLeuLysGlyGlu

                      SacII
841  ACCACCACCGAGGCCGTGGACGCCGCCACCGCGGAGAAGGTGTTCAAACAATACGC
     54▶ThrThrThrGluAlaValAspAlaAlaThrAlaGluLysVal IPheLysGlnTyrAl
897  TAATGACAACGGGGTCGACGGCGAGTGGACTTACGACGACGCCACCAAGACCTTCA
     72▶aAsnAspAsnGlyValAspGlyGluTrpThrTyrAspAspAlaThrLysThrPheT
                      AvaI
                 2x Protein G
953  CCGTGACCGAGAAGCCCGAGGTGATCGATGCCAGCGAGCTGACCCCCGCCGTGACC
     91▶hrValThrGluLysProGluVal I IeAspAlaSerGluLeuThrProAlaValThr
1009 ACCTACAAGCTAGTGATCAACGGCAAGACCCTGAAGGGCGAGACCACCACCGAGGC
     110▶ThrTyrLysLeuVal I IeAsnGlyLysThrLeuLysGlyGluThrThrThrGluAl
                      SacII
1065 CGTGGACGCCGCCACCGCGGAGAAGGTGTTCAAACAATACGCTAATGACAACGGGG
     128▶aValAspAlaAlaThrAlaGluLysValPheLysGlnTyrAlaAsnAspAsnGlyV
```

Figure 3B (cont'd I)

REPLACEMENT SHEET

```
                                                                                  NotI
1121  TCGACGGCGAGTGGACTTACGACGACGCCACCAAGACCTTCACCGTGACCGAGGCG
147▶ alAspGlyGluTrpThr TyrAspAspAlaThr LysThr PheThr Val Thr GluAla

                                                                                  myc
1177  GCCGCAGAACAAAAACTCATCTCAGAAGAGGATCTGAATGGGGCCGTCGACGAACA
166▶AlaAlaGluGlnLysLeulleSer GluGluAspLeuAsnGlyAlaVal AspGluGln

                      BsmI
1233  AAAACTCATCTCAGAAGAGGATCTGAATGCTGTGGGCCAGGACACGCAGGAGGTCA
184▶ nLysLeul leSer GluGluAspLeuAsnAla Val GlyGlnAspThr GlnGluVal l

1289  TCGTGGTGCCACACTCCTTGCCCTTTAAGGTGGTGGTGATCTCAGCCATCCTGGCC
203▶ leVal Val Pr oHis Ser LeuPr oPheLysVal Val Val l leSerAla l leLeuAla

                  TM  domain
1345  CTGGTGGTGCTCACCATCATCTCCCTTATCATCCTCATCATGCTTGGCAGAAGAA
222▶ LeuVal Val LeuThr l le l leSer Leul le l leLeul leMetLeuTr pGlnLysLy

          PvuI                       XbaI
1401  GCCACGTTCGTCGGCCGATCGAGAATCCATCTAGAGCTATTCTATAGTGTCACCTA
240▶ sPr oAr gSer SerAlaAspAr gGluSer l le●●●  ━━

          SacI
1457  AATGCTAGAGCTCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGT

                                                                                  poly  A
1513  TGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCC

1569  TTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATT

                                                    BbsI
1625  CTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAG

1681  GCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGTGGCG

                                                    AflIII
1737  GTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAA
1793  AGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA

1849  GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGA

1905  AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCG

1961  CTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGG

2017  GAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTC

                      ApaLI                              Col E1
2073  GTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGC

2129  CTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC

          AlwNI
2185  TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACA

2241  GAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTAT

2297  CTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCG

2353  GCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACG

2409  CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC
```

Figure 3B (cont'd II)

REPLACEMENT SHEET

BspHI
2465 TCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGA
2521 TCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATA
                                        EcoO109I
        Bsu36I   AlwNI
2577 TATGAGTAACCTGAGGCTATGGCAGGGCCTGCCGCCCCGACGTTGGCTGCGAGCCC

2633 TGGGCCTTCACCCGAACTTGGGGGGTGGGGTGGGGAAAAGGAAGAAACGCGGGCGT

2689 ATTGGCCCCAATGGGGTCTCGGTGGGGTATCGACAGAGTGCCAGCCCTGGGACCGA

                    TK poly A
2745 ACCCCGCGTTTATGAACAAACGACCCAACACCGTGCGTTTTATTCTGTCTTTTTAT

2801 TGCCGTCATAGCGCGGGTTCCTTCCGGTATTGTCTCCTTCCGTGTTTCAGTTAGCC

        AvrII
2857 TCCCCCTAGGGTGGGCGAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATC

2913 CAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGT
                                                    BstBI
2969 GGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACC
3025 CCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCG
            2634 •••PhePheGluAspLeuLeuArgTyrPheAIaIIeArgGInSe
3081 AATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCA
    2484rAspProAIaAIaIIIeGIyTyrLeuVaILeuPheArgAspAIaTrpGIuGIyGIyL
    SapI   RsrII
3137 AGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCAC
    2294euGIuGIuAIIaIIeAspArgThrAIaLeuAIaIIeAspGInTyrArgAspAIaVaI
3193 ACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATAT
    2114GIyLeuArgGIyCysAspIIePheGIySerPheArgGIyAsnGIuVaIMetIIeAs
3249 TCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCTC
    1924nProLeuCysAIaAspGIyHIsThrVaIVaILeuAspGIuGIyAspProMetSerA
3305 GCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTGATCATC
    1734IaLysLeuArgGIaPheLeuGIuAIaProAIaLeuGIyGInHIsGIuGInAspAsp
3361 CTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCG
    1554GInAspVaILeuGIyAIaGIuMetArgThrArgAIaArgGIuIIeArgHIsLysAI
3417 CTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCCATTGCA
    1364aGInHIsAspPheProCysThrAIaProAspLeuThrHIsLeuArgArgMetAIaA
3473 TCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTG
    1174spAIaMetIIeSerVaILysGIuAIaProAIaLeuHIsSerSerLeuLeuAspGIn
                                                    Tth111I
3529 CCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGA
    994GIyProVaIGIuGIyLeuLeuLeuTrpAspArgGIyAIaGIuThrVaIVaIAspLe
                            Neo-R.
    PvuIIFspI   MscI
3585 GCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTCG
    804uVaIAIaAIaCysProVaIGIyThrThrAIaLeuTrpSerLeuArgAIaAIaGIuA
                                                    NarI
3641 TCTTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCG
    614spGInLeuGIuAsnLeuAIaGIySerLeuAspThrLysVaIPheLeuVaIProArg
3697 CCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTG
    434GIyGInAIaSerLeuArgPheVaIAIaAIaAspSerCysGIyIIeThrGInGInAI
3753 CCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAAT
    244aTrpAspTyrGIyPheLeuArgGIuVaITrpAIaAIaProSerGIyAIaHIsLeuG
                            BsaBI
3809 CCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCGATCTTTGC
    54IyAspGInGIuIIeMet
            StuI
        AvrII   BseRI
3865 AAAAGCCTAGGCCTCCAAAAAAGCCTCCTCACTACTTCTGGAATAGCTCAGAGGCC

Figure 3B (cont'd III)

REPLACEMENT SHEET

```
        BseRI
3921  GAGGAGGCGGCCTCGGCCTCTGCATAAATAAAAAAAATTAGTCAGCCATGGGGCGG


                                         SV40 ori & Promotor
3977  AGAATGGGCGGAACTGGGCGGAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGA

                       Nsil
4033  CTATGGTTGCTGACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAG

                  SexAl                         Nsil
4089  CCTGGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGCATACT

                                                            Pvul
4145  TCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGACACACATTCCACA

      Ssu36I
4201  GCTGGTTCTTTCCGCCTCAGGACTCTTCCTTTTTCAATAAATCAATCTAAAGTATA
4257  TATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTC
              2874 •••TrpHisLysIIeLeuSerAIaGIyIIeGIu
                                        Eam11051
4313  AGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAA
      2764AIaIIeGInArgAsnArgGIuAspMetThrAIaGInSerGIyThr Thr Tyr IIeVa
4369  CTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGAC
      25741 Val I I IeArgSer Pr oLysGI yAspPr oGIyLeuAIaAIaIIeI IeGIyArgSer G
4425  CCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGA
      23841 yArgGIuGIyAIaGIySer LysAspAIaI IePheTrpGIyAIaProLeuAIaSer
4481  GCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCC
      2204ArgLeuLeuProGIyAIaValLysAspAIaGIuMetTrpAsp IIeLeuGInGInAr
                                          Fspl   Psp1406I
4537  GGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATT
      2014gSerAIaLeuThr LeuLeuGIuGIyThr LeuLeuLysArgLeuThr ThrAIaMetA
4593  GCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGG
      18241 aVaI ProMet Thr ThrAspArgGIuAspAsnProI IeAIaGIuAsnLeuGIuPro
4649  TTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTA
      1644GIuTrpArgAspLeuArgThr VaI HisAspGIyMetAsnHisLeuPheAIaThr Le
           Pvul
4705  GCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTC
      14544uGIuLysProGIyGIyI IeThr Thr LeuLeuLeuAsnAIaAIaAIaThrAsnAspSerM
                                                              bla
4761  ATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTT
      12644etThrIIeAIaAIaSer CysLeuGIuArgVaI ThrMetGIyAspThr LeuHisLys
            Scal
4817  TTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGAC
      1084GIuThr VaI ProSer Tyr GIuVaI LeuAspAsnGInSer Tyr HisI IeArgArgGI
4873  CGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACT
      894yLeuGInGIuGInGIyAIaAsp IIeArgSer LeuVaI AIaGIyCysLeuLeuVaI L
           Psp1406I
4929  TTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTT
      704ysPheThr SerMet MetPr oPheArgGIuGIuProArgPheSer GIuLeuI IeLys
                                          ApaLI
4985  ACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAG
      524GIySerAsnLeuAspLeuGIuI IeTyr GIyVaIArgAIaGIyLeuGInAspGIuAI
5041  CATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCC
      334aAspLysVaI LysVaI LeuThr GIuProHisAIaPheVaI ProLeuCysPheAIaA
5097  GCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTT
      144I aPhePheProI IeLeuAIaVaIArgPheHisGInIIeSerMet
          Sspl                                BspHI
5153  TCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTG
5209  AATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTG
5265  CCACCTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCG
```

Figure 3B (cont'd IV)

REPLACEMENT SHEET

```
                    Stem loop A
     5321  CAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCC


     5377  CTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTC



              f1  IR            Stem loop B
     5433  CCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTA


                  DraIII          Stem loop C        Primer-RNA
     5489  GGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGA



              Start Transcription
              VS-Synthese Nicking site  Stem loop D   _    Stem loop E
     5545  CGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTC


     5601  AACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTA

                            Apol          Apol            Sspl
     5657  TTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAATAT

     5713  TAACGCTTACAATTTAC
```

Figure 3B (cont'd V)